L Number	Hits	Search Text	DB	Time stamp
1	40339	li.in. or gruber.in. or jessee.in. or lin.in.	USPAT; US-PGPUB; EPO	2004/09/07 15:33
2	43361	(DNA or RNA or "nucleic acid") same (primer or probe) same hybridiz$5	USPAT; US-PGPUB; EPO	2004/09/07 15:34
3	6614	((DNA or RNA or "nucleic acid") same (primer or probe) same hybridiz$5) same biotin	USPAT; US-PGPUB; EPO	2004/09/07 15:34
4	5000	((DNA or RNA or "nucleic acid") same (primer or probe) same hybridiz$5) same transform$5	USPAT; US-PGPUB; EPO	2004/09/07 15:34
9	400	"uracil DNA glycolase" or UDG	USPAT; US-PGPUB; EPO	2004/09/07 15:34
13	9087	((DNA or RNA or "nucleic acid") same (primer or probe) same hybridiz$5) same ("single strand" or "single stranded")	USPAT; US-PGPUB; EPO	2004/09/07 15:34
15	1480	degenerate WITH probe	USPAT; US-PGPUB; EPO	2004/09/07 15:34
16	0	((degenerate WITH probe) WITH (library or libraries)) SAME biotin	USPAT; US-PGPUB; EPO	2004/09/07 15:34
20	189	"degenerate probe"	USPAT; US-PGPUB; EPO	2004/09/07 15:34
21	0	"degenerate probe"110 SAME screen	USPAT; US-PGPUB; EPO	2004/09/07 15:34
5	58	(((DNA or RNA or "nucleic acid") same (primer or probe) same hybridiz$5) same biotin) same nuclease	USPAT; US-PGPUB; EPO	2004/09/07 15:34
6	9	(((DNA or RNA or "nucleic acid") same (primer or probe) same hybridiz$5) same biotin) same UDG	USPAT; US-PGPUB; EPO	2004/09/07 15:34
7	3	(((DNA or RNA or "nucleic acid") same (primer or probe) same hybridiz$5) same biotin) same "nucleotide analog"	USPAT; US-PGPUB; EPO	2004/09/07 15:34
8	27	(((DNA or RNA or "nucleic acid") same (primer or probe) same hybridiz$5) same biotin) same ((circular)with(DNA or RNA or "nucleic acid"))	USPAT; US-PGPUB; EPO	2004/09/07 15:34
10	16	("uracil DNA glycolase" or UDG) same biotin	USPAT; US-PGPUB; EPO	2004/09/07 15:34
11	37	("uracil DNA glycolase" or UDG) same ((DNA or RNA or "nucleic acid") same (primer or probe) same hybridiz$5)	USPAT; US-PGPUB; EPO	2004/09/07 15:34
12	9	("uracil DNA glycolase" or UDG) same (((DNA or RNA or "nucleic acid") same (primer or probe) same hybridiz$5) same biotin)	USPAT; US-PGPUB; EPO	2004/09/07 15:34
14	3	(((DNA or RNA or "nucleic acid") same (primer or probe) same hybridiz$5) same ("single strand" or "single stranded")) same ("uracil DNA glycolase" or UDG)	USPAT; US-PGPUB; EPO	2004/09/07 15:34
17	76	((degenerate WITH probe) WITH (library or libraries)) and biotin	USPAT; US-PGPUB; EPO	2004/09/07 15:34
18	275	(degenerate WITH probe) WITH (library or libraries)	USPAT; US-PGPUB; EPO	2004/09/07 15:34
19	1	5989867.pn.	USPAT; US-PGPUB; EPO	2004/09/07 15:34
22	15	"degenerate probe" SAME screen	USPAT; US-PGPUB; EPO	2004/09/07 15:34

23	1088	(li.in. or gruber.in. or jessee.in. or lin.in.) and ((DNA or RNA or "nucleic acid") same (primer or probe) same hybridiz$5)	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/09/07 15:34
24	234	((li.in. or gruber.in. or jessee.in. or lin.in.) and ((DNA or RNA or "nucleic acid") same (primer or probe) same hybridiz$5)) and (((DNA or RNA or "nucleic acid") same (primer or probe) same hybridiz$5) same ("single strand" or "single stranded"))	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/09/07 15:36
25	31	(((li.in. or gruber.in. or jessee.in. or lin.in.) and ((DNA or RNA or "nucleic acid") same (primer or probe) same hybridiz$5)) and (((DNA or RNA or "nucleic acid") same (primer or probe) same hybridiz$5) same ("single strand" or "single stranded"))) and hapten	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/09/07 15:43
26	64625	"single stranded" or (single NEAR2 strand$)	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/09/07 15:43
27	43479	("single stranded" or (single NEAR2 strand$)) WITH (DNA or RNA or "nucleic acid")	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/09/07 15:44
28	17194	(("single stranded" or (single NEAR2 strand$)) WITH (DNA or RNA or "nucleic acid")) SAME (hybridiz$ or ligand or hapten or biotin or streptavidin)	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/09/07 15:45
29	9205	((("single stranded" or (single NEAR2 strand$)) WITH (DNA or RNA or "nucleic acid")) SAME (hybridiz$ or ligand or hapten or biotin or streptavidin)) SAME (double NEAR2 strand$)	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/09/07 15:46
30	4074	((((("single stranded" or (single NEAR2 strand$)) WITH (DNA or RNA or "nucleic acid")) SAME (hybridiz$ or ligand or hapten or biotin or streptavidin)) SAME (double NEAR2 strand$)) and (probe NEAR3 target)	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/09/07 15:46
31	1636	(((((("single stranded" or (single NEAR2 strand$)) WITH (DNA or RNA or "nucleic acid")) SAME (hybridiz$ or ligand or hapten or biotin or streptavidin)) SAME (double NEAR2 strand$)) and (probe NEAR3 target)) and circular	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/09/07 15:46
32	47	((((((("single stranded" or (single NEAR2 strand$)) WITH (DNA or RNA or "nucleic acid")) SAME (hybridiz$ or ligand or hapten or biotin or streptavidin)) SAME (double NEAR2 strand$)) and (probe NEAR3 target)) and circular) and "circular target"	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/09/07 15:56
33	4	4873192.pn. or 5035966.pn.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/09/07 16:09
34	0	hartley.in. and phagemide and "single-stranded"	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/09/07 16:09
35	0	hartley.in. and phagemide	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/09/07 16:09
36	11	hartley.in. and phagemid and "single-stranded"	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/09/07 16:10

37	2670	hartley.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/09/07 16:10
38	11	hartley.in. and "single strand"	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/09/07 16:39
39	131864	M13	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/09/07 16:39
40	7022	M13 SAME phage	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/09/07 16:39
41	372	conver$6 NEAR6 "double strand"	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/09/07 16:40
42	122	(M13 SAME phage) and (conver$6 NEAR6 "double strand")	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/09/07 16:40
43	95	((M13 SAME phage) and (conver$6 NEAR6 "double strand")) and "single strand"	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/09/07 16:40
44	85	(((M13 SAME phage) and (conver$6 NEAR6 "double strand")) and "single strand") and library	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/09/07 16:40
45	81	((((M13 SAME phage) and (conver$6 NEAR6 "double strand")) and "single strand") and library) and (hapten or ligand or biotin)	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/09/07 16:52
46	2	5482845.pn.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/09/07 16:48
47	0	(conver$6 NEAR6 "double strand") WITH M13	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/09/07 16:52
48	23	(conver$6 NEAR6 "double strand") SAME M13	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/09/07 17:38
49	2	6274320.pn.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/09/07 17:39
50	2	6329150.pn.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/09/07 17:39

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FILE 'MEDLINE, EMBASE, BIOSIS, CAPLUS' ENTERED AT 16:58:13 ON 07 SEP 2004
L1          2887 S TARGET (5A) "NUCLEIC ACID"
L2        610654 S LI-W?/AU OR GRUBER?/AU OR JESSEE?/AU OR LIN?/AU
L3       4096252 S "NUCLEIC ACID" OR DNA OR RNA
L4          2518 S PROBE (S) SINGLE-STRAND?
L5          2270 S L3 (P) L4
L6            25 S L5 AND L2
L7            17 DUP REM L6 (8 DUPLICATES REMOVED)
L8             7 S L7 NOT PY>=1996
L9         11619 S M13
L10          302 S CONVER? (3A) "DOUBLE STRAND"
L11            7 S L10 AND L9
L12            3 DUP REM L11 (4 DUPLICATES REMOVED)
L13       563441 S HYBRIDIZ?
L14         4996 S L13 (3A) SELECT?
L15           51 S L1 AND L14
L16            3 S L15 NOT PY>=1996
L17           39 S L14 AND L4
L18           25 DUP REM L17 (14 DUPLICATES REMOVED)
L19           14 S L18 NOT PY>=1996
L20       665629 S HAPTEN OR LIGAND OR BIOTIN OR STREPTAVIDIN
L21          225 S L4 (P) L20
L22            6 S L21 AND L1
L23            6 DUP REM L22 (0 DUPLICATES REMOVED)
L24           38 S ENRICH? (5A) "SINGLE STRAND"
L25           15 DUP REM L24 (23 DUPLICATES REMOVED)
L26            2 S L25 NOT PY>=1996
L27        25770 S DNA (2A) LIBRAR?
L28           38 S L27 AND L4
L29           30 DUP REM L28 (8 DUPLICATES REMOVED)
L30           19 S L29 NOT PY>=1996
L31          299 S L20 AND "DOUBLE STRAND"
L32            0 S L30 AND "DOUBLE STRAND"
L33            3 S L30 AND L20
L34           11 S CIRCUL? (3A) L1
L35           11 DUP REM L34 (0 DUPLICATES REMOVED)
L36         1062 S "PLASMID LIBRARY"
L37            6 S L36 AND "SINGLE STRAND"
L38            4 DUP REM L37 (2 DUPLICATES REMOVED)
L39        49161 S LIBRARY (S) L3
L40           87 S L39 AND L4
L41           58 S L40 AND HYBRID?
L42           49 S L41 NOT PY>=1998
L43           36 DUP REM L42 (13 DUPLICATES REMOVED)
L44            7 S "SINGLE STRAND" AND L43
L45        15054 S L39 AND HYBRIDI?
L46           45 S L45 AND "SINGLE STRAND"
L47           34 DUP REM L46 (11 DUPLICATES REMOVED)
L48           16 S L47 NOT PY>=1996
L49        85173 S TARGET (S) (SEQUENCE OR DNA OR RNA OR "NUCLEIC ACID")
L50          708 S L49 (S) ENRICH?
L51          143 S L50 NOT PY>=1994
L52          109 DUP REM L51 (34 DUPLICATES REMOVED)
L53            0 S L52 AND "SINGLE STRAND"
L54            0 S L52 AND (SINGLE (2A) STRAND)
L55            1 S L52 AND "DOUBLE STRAND"
L56           10 S L52 AND L20
L57           10 DUP REM L56 (0 DUPLICATES REMOVED)
L58            1 S L57 AND HYBRIDI?
```

ANSWER 11 OF 14 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1990:453728 CAPLUS
DOCUMENT NUMBER: 113:53728
TITLE: Novel high efficiency cDNA cloning vectors for synthesis of single stranded cDNA and enhancement of specific sequences by **hybridization/selection**
INVENTOR(S): Pruitt, Steven C.
PATENT ASSIGNEE(S): Health Research, Inc., USA
SOURCE: Eur. Pat. Appl., 21 pp.
CODEN: EPXXDW
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
EP 346877	A1	19891220	EP 1989-110816	19890614
R: AT, BE, CH, DE, ES, FR, GB, GR, IT, LI, LU, NL, SE				
CA 1335428	A1	19950502	CA 1989-602526	19890612
AU 8936313	A1	19900201	AU 1989-36313	19890614
AU 619303	B2	19920123		
JP 02186991	A2	19900723	JP 1989-153534	19890614
US 5238834	A	19930824	US 1992-890355	19920522
PRIORITY APPLN. INFO.:			US 1988-206426	19880614

AB CDNA cloning vectors containing a prokaryotic origin of replication, a BstXI site, the intergenic region of bacteriophage f1, and a selectable marker for high efficiency cDNA cloning are described. Unlike vectors of the prior art, the cDNA cloning vectors permit recircularization of the linear form of a recombinant DNA mol. containing cDNA by intramol. ligation and self-priming of second strand cDNA synthesis. These vectors can also be recovered as a single-stranded form making them useful as hybridiz

ANSWER 8 OF 11 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2000:421337 CAPLUS
DOCUMENT NUMBER: 133:69768
TITLE: Amplification of circularized nucleic acid probes
INVENTOR(S): Hafner, Gregory John; Giffard, Phillip Morrison; Wolter, Lindsay Collin; Dale, James Langham; Stafford, Mark Richard; Yang, Ilin Chen Hai-ni; Voisey, Joanne
PATENT ASSIGNEE(S): Diatech Pty. Ltd., Australia
SOURCE: PCT Int. Appl., 102 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000036141	A1	20000622	WO 1999-AU1110	19991214

W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, T

L35 ANSWER 6 OF 11 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2001:208461 CAPLUS
DOCUMENT NUMBER: 134:247918
TITLE: Method of sequencing a nucleic acid
INVENTOR(S): Rothberg, Jonathan M.; Bader, Joel S.; Dewell, Scott B.; McDade, Keith; Simpson, John W.; Berka, Jan; Colangelo, Christopher M.
PATENT ASSIGNEE(S): Curagen Corporation, USA
SOURCE: PCT Int. Appl., 67 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 3
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001020039	A2	20010322	WO 2000-US25290	20000915
WO 2001020039	A3	20020321		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
US 6274320	B1	20010814	US 1999-398833	19990916
EP 1212467	A2	20020612	EP 2000-965029	20000915
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL				

JP 2003514514 T2 20030422 JP 2001-523808 20000915
US 2002012933 A1 20020131 US 2001-826141 20010404
PRIORITY APPLN. INFO.: US 1999-398833 A2 19990916
WO 2000-US25290 W 20000915

AB Methods and apparatuses for sequencing a nucleic acid are disclosed. In one aspect, the method includes annealing a population of circular nucleic acid mols. to a plurality of anchor primers linked to a solid support, and amplifying those members of the population of **circular nucleic acid** mols. which anneal to the **target** nucleic acid, and then sequencing the amplified mols. by detecting the presence of a sequence byproduct such as pyrophosphate.

WER 1 OF 7 MEDLINE on STN
ACCESSION NUMBER: 87305178 MEDLINE
DOCUMENT NUMBER: PubMed ID: 3622924
TITLE: Expression of myosin heavy chain gene in the sea urchin: coregulation with muscle actin transcription in early development.
AUTHOR: Rose S J 3rd; Rosenberg M J; Britten R J; Davidson E H
CONTRACT NUMBER: GM-20927 (NIGMS)
SOURCE: Developmental biology, (1987 Sep) 123 (1) 115-24. Journal code: 0372762. ISSN: 0012-1606.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198709
ENTRY DATE: Entered STN: 19900305
Last Updated on STN: 19970203
Entered Medline: 19870929

AB A fragment of a Strongylocentrotus purpuratus (Sp) myosin heavy chain (MHC) gene was isolated from a genomic recombinant **DNA library** by cross-reaction with a cloned Drosophila melanogaster (Dm) MHC probe. A portion of a 227-nucleotide Sp coding sequence that is included in this fragment predicts a peptide very closely homologous with a region of the Dm sequence. The MHC gene sequence is present in a single copy per haploid Sp genome, and the gene is utilized in adult as well as embryonic muscle. The quantity of MHC transcript was measured in embryos of various stages by **single-strand** RNA **probe** excess titration. Transcripts are not observed until postgastrular stages, after which they accumulate rapidly. The time course of accumulation closely parallels that measured earlier for muscle actin message.

L44 ANSWER 2 OF 7 EMBASE on STN
ACCESSION NUMBER: 95151878 EMBASE
DOCUMENT NUMBER: 1995151878
TITLE: Isolation and characterization of the gene encoding the surface membrane 3'-nucleotidase/nuclease of Leishmania donovani.
AUTHOR: Debrabant A.; Gottlieb M.; Dwyer D.M.
CORPORATE SOURCE: Laboratory of Parasitic Diseases, Nat. Inst. Allergy/Infectious Dis., National Institutes of Health,Bethesda, MD 20892-0425, United States
SOURCE: Molecular and Biochemical Parasitology, (1995) 71/1 (51-63).
ISSN: 0166-6851 CODEN: MBIPDP
COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 004 Microbiology
LANGUAGE: English
SUMMARY LANGUAGE: English

AB Leishmania donovani and related trypanosomatid protozoa possess an externally oriented surface membrane enzyme capable of hydrolyzing both 3'-nucleotides and nucleic acids. By virtue of these activities, this 3'-nucleotidase/nuclease (3'-NT/Nu), previously shown to be analogous to fungal and plant class-I **single-strand**-specific nucleases, is thought to play a critical role in the salvage of purines, essential for the survival of these organisms. The 43-kDa 3'-NT/Nu was purified from L. donovani promastigotes and trypsin treated. Four of the released tryptic peptide fragments yielded amino-acid sequence information (Pept-1 to Pept-4) which provided the basis for the preparation of oligonucleotide primers used for PCR amplification of an approx. 300-bp **DNA** fragment. This fragment was cloned, sequenced and used to

probe a genomic L. donovani cosmid **library**. Nucleotide sequence analysis of a 4.5-kb SmaI fragment, isolated from a cosmid clone, revealed an open reading frame (ORF) of 1434 nt encoding a 477-amino-acid protein. Pept-1 to Pept-4 were mapped onto the ORF-deduced protein sequence. Peptides corresponding to Pept-1 to Pept-4 were synthesized and used to immunize rabbits. The resulting anti-peptide antibodies recognized the 43-kDa protein on Western blots and immunoprecipitated the native 3'-nucleotidase activity from L. donovani membrane extracts. Further, the ORF-deduced protein shared significant sequence identity with the S1 and P1 fungal nucleases of Aspergillus oryzae and Penicillium citrinum, respectively. Cumulatively, these results demonstrated that the ORF corresponded to a gene for the L. donovani 3'-nucleotidase/nuclease. In Northern blots a nucleotide **probe** specific for the 3'-NT/Nu gene **hybridized** to a single 2.5-kb messenger **RNA**. Results of Southern blot analyses were consistent with the 3'-NT/Nu being encoded by a single copy gene. These data constitute the first report of the gene for this unique trypanosomatid surface membrane enzyme.

L44 ANSWER 3 OF 7 EMBASE
on STN

ACCESSION NUMBER: 94326061 EMBASE
DOCUMENT NUMBER: 1994326061
TITLE: The isolation of novel intracellular factors by differential screening methods.
AUTHOR: Tohda C.; Nomura Y.
CORPORATE SOURCE: Department of Applied Biochemistry, Research Institute for Wakan-yaku, Toyama Med. and Pharm. University,Toyama 930-01, Japan
SOURCE: Folia Pharmacologica Japonica, (1994) 104/4 (285-291). ISSN: 0015-5691 CODEN: NYKZAU
COUNTRY: Japan
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 008 Neurology and Neurosurgery
022 Human Genetics
029 Clinical Biochemistry
030 Pharmacology
037 Drug Literature Index
LANGUAGE: Japanese
SUMMARY LANGUAGE: English

AB Synaptic plasticity, a physiological basis of learning and memory, is mainly classified into two categories: 1) relatively short-term changes in electrical activities and 2) more long-lasting morphological changes in synapses. Studies on neuronal differentiation have provided detailed clarification of many of the morphological changes in synapses. Although it has been demonstrated that neuronal differentiation is induced by a variety of stimuli, the mechanism of neuronal differentiation has never been sequentially understood. Since there must be unknown factors relevant to these complicated processes, it is important to find and identify the novel intracellular factors that are able to induce the differentiation of neurons. Differential screening is useful cloning method to identify molecules without any information about their structures. Genes expressed in a distinct pattern among two or more groups, eg. different drug-treated cells, tissues and so on, can be isolated. To identify novel neuronal differentiation factors, we differentially screened approximately 500,000 primary clones from the cDNA **library** of NG108-15 cells treated with TPA and diBu-cAMP for 72 hr. Using two **single strand** cDNA probes, which were reverse-transcribed from poly(A)+ **RNA**, TA-20 was isolated from cells treated with TPA and diBu-cAMP (**probe** TA) or from cells treated with diBu-cAMP alone (**probe** A) for 72 hr. Clones that **hybridized** preferentially to the **probe** TA were further investigated by Southern and Northern blots. Thus the identified clone TA20 is a novel gene and plays functional roles as a neuronal differentiation factor.

L44 ANSWER 4 OF 7 EMBASE COPYRIGHT 2004 ELSEVIER INC. ALL RIGHTS RESERVED. on STN
ACCESSION NUMBER: 94167073 EMBASE
DOCUMENT NUMBER: 1994167073
TITLE: Cloning and characterization of a single-stranded DNA binding protein that specifically recognizes deoxycytidine stretch.
AUTHOR: Ito K.; Sato K.; Endo H.
CORPORATE SOURCE: Department of Molecular Biology, School of Life Sciences, Faculty of Medicine, Tottori Univ,Yonago 683, Japan
SOURCE: Nucleic Acids Research, (1994) 22/1 (53-58).
ISSN: 0305-1048 CODEN: NARHAD
COUNTRY: United Kingdom
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 022 Human Genetics
029 Clinical Biochemistry
LANGUAGE: English
SUMMARY LANGUAGE: English
AB We previously identified a G-rich silencer element involved in negative regulation of catalase gene expression in some hepatoma cells. To study a nuclear binding protein for this element, we screened cDNA libraries from a rat ascites hepatoma cell line by binding with a synthetic oligonucleotide **probe** and obtained several clones. One of them, designated SW, was studied in detail. A clone (SW2) of this series contained a near full length cDNA encoding a putative peptide with 463 amino acid residues. We isolated this peptide as a fusion protein. It was found that the protein strongly bound to the C-stretch of the DNA sequence in a **single strand** specific fashion, but absolutely did not to G-rich sequence. The protein bound weakly to the corresponding double-stranded DNA as well as to G-rich RNA sequence. This protein, though not the expected one, was found to be a novel protein whose DNA binding domain was located on the region containing at least 75 amino acid residues of the carboxyl terminus. A proline rich region was also observed in the middle part of the protein. Northern blot profiles indicated extensive and slight expression of both 2.0 kb and 2.7 kb mRNA species in some hepatoma cell lines and in the rat liver, respectively.

L44 ANSWER 5 OF 7 EMBASE COPYRIGHT 2004 ELSEVIER INC. ALL RIGHTS RESERVED. on STN
ACCESSION NUMBER: 94106551 EMBASE
DOCUMENT NUMBER: 1994106551
TITLE: Identification and cDNA cloning of single-stranded DNA binding proteins that interact with the region upstream of the human c-myc gene.
AUTHOR: Negishi Y.; Nishita Y.; Saegusa Y.; Kakizaki I.; Galli I.; Kihara F.; Tamai K.; Miyajima N.; Iguchi-Ariga S.M.M.; Ariga H.
CORPORATE SOURCE: Faculty of Pharmaceutical Sciences, Hokkaido University, Kita 12 Nishi 6,Kita-ku, Sapporo 060, Japan
SOURCE: Oncogene, (1994) 9/4 (1133-1143).
ISSN: 0950-9232 CODEN: ONCNES
COUNTRY: United Kingdom
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 022 Human Genetics
LANGUAGE: English
SUMMARY LANGUAGE: English
AB We have previously reported that a c-myc protein complex binds to the region upstream of the c-myc gene, where exist an origin of cellular **DNA** replication (ori) and a transcriptional enhancer. Both functions require a 21 bp long sequence, while the c-myc protein complex recognizes a 7 bp consensus therein. It was recently reported that **single-stranded DNA** binding proteins bound

specifically to sequences that play roles in **DNA** replication or transcription. We examined for proteins binding to the **single-stranded** DNAs of the 21 bp element (myc(H-P)21). In a band shift assay with HL60 cells nuclear extract, probes of either the plus strand or the minus strand gave rise to specific signals. Mutation introduced within a short consensus ((A)/(T)CT(A)/(T)(A)/(T)T) present in both strands completely abolished binding in either case. Southwestern blotting analysis showed that proteins of molecular weight 105, 80, 50, 45, 40, 39.5 and 14 k Da bound sequence-specifically to either strand and 22 kDa to minus strand to the cognate (A)/(T)CT(A)/(T)(A)/(T)T consensus. These **single-stranded DNA** binding proteins were named MSSP, c-myc gene **single strand** binding proteins. We attempted to isolate the cDNAs encoding these proteins by screening a human cDNA **library** with the plus **single-stranded** oligonucleotide as a **probe**. Among several positive clones, we have characterized one, termed MSSP-1. MSSP-1 produced in E. coli as a fusion protein with GST specifically interacted with **single-stranded** TCTTAT (plus myc(H-P)21) and ACTATT (in minus myc(H-P)21), the consensus of which can be referred to as (A)/(T)CT(A)/(T)A/(T)T. Sequence analysis of MSSP-1 cDNA revealed that two domains thereof are homologous to the **RNA** binding motifs common to several ribonucleoproteins. Interestingly, the MSSP-1/ GST fusion protein specifically recognized myc(H-P)21 not only in **single-stranded** but also in double-stranded forms. Binding properties of MSSP-1 imply its functions in **DNA** replication. Furthermore, when the AT stretch in the SV40 ori core was substituted by TCTTAT, MSSP-1 promoted viral **DNA** replication depending on the consensus sequences.

L44 ANSWER 6 OF 7 EMBASE COPYRIGHT 2004 ELSEVIER INC. ALL RIGHTS RESERVED. on STN

ACCESSION NUMBER: 91006074 EMBASE
DOCUMENT NUMBER: 1991006074
TITLE: Molecular cloning of the human XRCC1 gene, which corrects defective DNA strand break repair and sister chromatid exchange.
AUTHOR: Thompson L.H.; Brookman K.W.; Jones N.J.; Allen S.A.; Carrano A.V.
CORPORATE SOURCE: Biomedical Sciences Division, Lawrence Livermore, National Laboratory, P.O. Box 5507,Livermore, CA 94550, United States
SOURCE: Molecular and Cellular Biology, (1990) 10/12 (6160-6171). ISSN: 0270-7306 CODEN: MCEBD4
COUNTRY: United States
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 022 Human Genetics
029 Clinical Biochemistry
LANGUAGE: English
SUMMARY LANGUAGE: English

AB We describe the cloning and function of the human XRCC1 gene, which is the first mammalian gene isolated that affects cellular sensitivity to ionizing radiation. The CHO mutant EM9 has 10-fold-higher sensitivity to ethyl methanesulfonate, 1.8-fold-higher sensitivity to ionizing radiation, a reduced capacity to rejoin **single-strand DNA** breaks, and a 10-fold elevated level of sister chromatid exchange compared with the CHO parental cells. The complementing human gene was cloned from cosmid **library** of a tertiary transformant. Two cosmid clones produced transformants that showed .apprx.100% correction of the repair defect in EM9 cells, as determined by the kinetics of strand break repair, cell survival, and the level of sister chromatid exchange. A nearly full-length clone obtained from the pcD2 human cDNA expression **library** gave .apprx.80% correction of EM9, as determined by the level of sister chromatid exchange. Based on an analysis of the nucleotide

sequence of the cDNA insert compared with that of the 5' end of the gene from a cosmid clone, the cDNA clone appeared to be missing .apprx.100 bp of transcribed sequence, including 26 nucleotides of coding sequence. The cDNA **probe** detected a single transcript of .apprx.2.2 kb in HeLa polyadenylated **RNA** by Northern (**RNA**) blot **hybridization**. From the open reading frame and the positions of likely start sites for transcription and translation, the size of the putative XRCC1 protein is 633 amino acids (69.5 kDa). The size of the XRCC1 gene is 33 kb, as determined by localizing the endpoints on a restriction endonuclease site map of one cosmid clone. The deduced amino acid sequence did not show significant homology with any protein in the protein sequence data bases examined.

L44 ANSWER 7 OF 7 EMBASE
on STN

ACCESSION NUMBER: 84019196 EMBASE
DOCUMENT NUMBER: 1984019196
TITLE: Physical characterization and molecular cloning of the Shope fibroma virus DNA genome.
AUTHOR: Wills A.; Delange A.M.; Gregson C.; et al.
CORPORATE SOURCE: Department of Biochemistry, University of Alberta, Edmonton, Alta., Canada
SOURCE: Virology, (1983) 130/2 (403-414).
CODEN: VIRLAX
COUNTRY: United States
DOCUMENT TYPE: Journal
FILE SEGMENT: 047 Virology
016 Cancer
LANGUAGE: English
AB **DNA** from several independent strains of Shope fibroma virus, a tumorogenic leporipoxvirus of rabbits, was isolated and analyzed by restriction endonuclease digestion and Southern blotting. The restriction profiles indicated a high degree of sequence conservation among the isolates but blotting under standard stringencies revealed no detectable cross homology with a member of the orthopoxvirus group, vaccinia. The genome of the fibroma virus was calculated to be in excess of 160 kilobases and shown to possess two features analogous to the orthopoxvirus group: (1) the terminal restriction fragments possess covalently closed hairpin structures; and (2) the terminal sequences are present as inverted repeats of greater than 10 kilobases. The terminal 3.6 kilobase BamHI restriction fragment was cloned in pBR322 after removal of the hairpin structure with mung bean **single strand**-specific endonuclease and addition of BamHI linkers. SFV sequences within this terminal region were shown, using 32P SFV cloned terminal **probe**, to have none of the sequence heterogeneity characteristic of vaccinia **DNA** termini. The remaining 20 internal SFV BamHi restriction fragments were propagated in bacterial plasmids either as intact fragments, or after secondary digestion with HindIII, and together constitute the complete cloned SFV sequence **library**.

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ACCESSION NUMBER: 90142156 EMBASE
DOCUMENT NUMBER: 1990142156
TITLE: A method for difference cloning: Gene amplification following subtractive **hybridization**.
AUTHOR: Wieland I.; Bolger G.; Asouline G.; Wigler M.
CORPORATE SOURCE: Cold Spring Harbor, Laboratory,Cold Spring Harbor, NY 11724, United States
SOURCE: Proceedings of the National Academy of Sciences of the United States of America, (1990) 87/7 (2720-2724). ISSN: 0027-8424 CODEN: PNASA6
COUNTRY: United States
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 022 Human Genetics
029 Clinical Biochemistry
LANGUAGE: English
SUMMARY LANGUAGE: English

AB We describe a procedure for genomic difference cloning, a method for isolating sequences present in one genomic **DNA** population ('tester') that is absent in another ('driver'). By subtractive **hybridization**, a large excess of driver is used to remove sequences common to a biotinylated tester, **enriching** the '**target**' sequences that are unique to the tester. After repeated subtractive **hybridization** cycles, tester is separated from driver by avidin/**biotin** affinity chromatography, and single-stranded **target** is amplified by the polymerase chain reaction, rendering it double-stranded and clonable. We model two situations: the gain of sequences that result from infection with a pathogen and the loss of sequences that result from a large hemizygous deletion. We obtain 100- to 700-fold **enrichment** of **target** sequences.

=> d his

(FILE 'HOME' ENTERED AT 16:57:00 ON 07 SEP 2004)

FILE 'MEDLINE, EMBASE, BIOSIS, CAPLUS' ENTERED AT 16:58:13 ON 07 SEP 2004
L1 2887 S TARGET (5A) "NUCLEIC ACID"
L2 610654 S LI-W?/AU OR GRUBER?/AU OR JESSEE?/AU OR LIN?/AU
L3 4096252 S "NUCLEIC ACID" OR DNA OR RNA
L4 2518 S PROBE (S) SINGLE-STRAND?
L5 2270 S L3 (P) L4

ANSWER 2 OF 3 MEDLINE on STN DUPLICATE 1
ACCESSION NUMBER: 82247814 MEDLINE
DOCUMENT NUMBER: PubMed ID: 6212928
TITLE: Identification of ColE1 DNA sequences that direct single strand-to-**double strand conversion** by a phi X174 type mechanism.
AUTHOR: Nomura N; Low R L; Ray D S
CONTRACT NUMBER: AI 10752-08 (NIAID)
SOURCE: Proceedings of the National Academy of Sciences of the United States of America, (1982 May) 79 (10) 3153-7. Journal code: 7505876. ISSN: 0027-8424.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198209
ENTRY DATE: Entered STN: 19900317
Last Updated on STN: 19970203
Entered Medline: 19820917

AB A DNA single-strand initiation sequence, named rriA (called rri-1 previously), was detected in the origin region (Hae II fragment E) of the ColE1 plasmid [Nomura, N. & Ray, D. S. (1980) Proc. Natl. Acad. Sci. USA 77, 6566-6570]. Another site, called rriB, has been found on the opposite strand of Hae II fragment C. Both rriA and rriB (i) direct conversion of chimeric **M13** phage single-stranded DNA to parental replicative form DNA in vivo by a rifampicin-resistant mechanism that is dependent on the dnaG and dnaB gene products, (ii) provide effector sites of dATP hydrolysis by primosomal protein n', and (iii) require the same primosomal proteins as phi X174 DNA for directing the in vitro conversion that rriA is the DNA sequence that determines the mechanism of lagging strand synthesis of ColE1 DNA and that the mechanism of discontinuous synthesis involves the primosomal proteins utilized in the in vitro